







Matches 356; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

560 CGAAGAGTTCTTCAAGCATATGATTGAGCAGACAGCAAGCTCAAGCGCTGATGACA 619  
 107 CCACAGAGTTCTTTAAGCAAGAACGTCCTTGAACTTCAGCAGCAGCAGCATACAGAGT 166  
 620 TGGGGCCGATCAAGCCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679  
 167 TGGGAGGGGTCAAGAGCAGCTTGGCTGTGTCTCTTGGGCTCTTCTTCATCGTCTACT 226  
 680 TCTCTTGTGGAAGAGAGTCAGAGAGTGTGCAAGAGTGTGCTGCTGCTGCTGCTGCT 739  
 227 TTGCGCTGTGGAAGGAGCAGACCTCTGCGAAGGCTGTGTGATCTGAGCCACCTTC 286  
 740 CGTAGCTGTGCTGTGATCTGTGCTGCGAGAGCGCTCAAGCTTCCAGAGCGAGAG 799  
 287 CCTAGCTGTGCTCTCTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346  
 800 GCATACGCTACTACTTACCTTACCCAGAGTGGCAGCAAAATGCAAACTTAAGTATGAT 859  
 347 GATATGCTACTACTGAGTCTCAGTGGAGAACTGTTGAACCTGGAGATCTGATG 406  
 860 ACGGCGCATCCCAAGATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919  
 407 CTGCGCGCGCCAGATTTTCTTCTCTAGGCGCCAGGTTTGGCTGCTGCTGCTGCT 466  
 920 CCAGCTACACAGATTAACAACAGCTACAGAGAGCGCTCATCTTCTTATCA 979  
 467 CTAGCTATACAGATTTCCACAACTGCTACAGAGAGCGCCCTGATCTACAGCAGCA 526  
 980 ACTGCTTACCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039  
 527 ACTGCTGACCGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586  
 1040 ACGTTCAGACAGAGCATCGAGAGGTTGGCTGGAAGCGCCCTGAGCTGCTGCT 1093  
 587 ATGTACACACAGAGCGGTGGAGACAGTGGCCAGACAGAGATGCGCTGATCT 640

Db

RESULT 4  
 AU131521 800 bp mRNA linear EST 01-AUG-2002  
 LOCUS AU131521 NT2RP3 Homo sapiens cDNA clone NT2RP3002722 5', mRNA  
 DEFINITION AU131521 NT2RP3 Homo sapiens cDNA clone NT2RP3002722 5', mRNA  
 sequence.  
 ACCESSION AU131521  
 VERSION AU131521  
 KEYWORDS GI:10991875  
 ORGANISM human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 800)  
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,  
 Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and  
 Isogai,T.  
 HRI human cDNA project  
 Unpublished (2000)  
 CONTACT: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3986  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix  
 Research Institute; cDNA library construction: Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.  
 Location/Qualifiers  
 1..800  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="NT2RP3002722"

BASE COUNT 128 a 235 c 229 g 204 t 4 others

Query Match 13.6%; Score 240.4; DB 9; Length 800;  
 Best Local Similarity 61.1%; Pred No. 2.3e-52;  
 Matches 385; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

600 GTCTACAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659  
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 660 GGTCTTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719  
 201 CTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260  
 720 GTGGGTGACAGCTGTGGCCCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779  
 261 GTACTTCACTGCTACATTCCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 320  
 780 GCTTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839  
 321 GCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 380  
 840 AACTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899  
 381 GTCCCTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 440  
 900 CGGAACCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959  
 441 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 500  
 960 GCTCATCATCTTCTTATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1019  
 501 CATCATCTGCTGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCT 560  
 1020 GGTTTTGGGATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1079  
 561 CATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 620  
 1080 CCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139  
 621 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 680  
 1140 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199  
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 1200 TCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1229  
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Db

RESULT 5  
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 LOCUS BO885751  
 DEFINITION AGENCOURT\_8753997 NIH\_MGC\_130 Mus musculus cDNA IMAGE:6332622  
 5', mRNA sequence.  
 ACCESSION BO885751  
 VERSION BO885751  
 KEYWORDS GI:2227769  
 EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)





TITLE	A large scale analysis of mRNAs expressed by primary mesenchyme cells of the sea urchin embryo			
JOURNAL MEDLINE	Development 128 (13), 2615-2627 (2001)			
COMMENT	Contact: Ettensohn CA Dept. Biol. Sci. Carnegie Mellon University 4400 Fifth Avenue, Pittsburgh, PA 15213, USA Tel: +1 412 268 5849 Email: ettensohn@andrew.cmu.edu. Location/Qualifiers 1. .798			
FEATURES	/organism="Strongylocentrotus purpuratus" /db_xref="taxon:7668" /clone="91222851_N20_072_PC_0020_B2_MR_G10" /clone_11b="Sea urchin primary mesenchyme cell cDNA library" /tissue_type="embryo" /cell_type="primary mesenchyme cells" /lab_host="E.coli" /note="vector: pSPOR1; Site_1: NotI; Site_2: SalI; oligo dt priming from poly A+ RNA; directionally cloned"			
BASE COUNT	136 a	241 c	184 g	236 t
ORIGIN	1 others			
Query Match	13.1%	Score 230.4	DB 12	Length 798
Best Local Similarity	57.3%	Pred. No. 1e-49		
Matches 434	Conservative 0	Mismatches 322	Indels 1	Gaps 1
Db	715 GTGGTGTGGGAGACGCTCTGGCCCCGACGTGGTGGCTGATTTCGCTGGCAGAGGC	774		
	42 GTGGTGTACCTCAGACGACTTCCCTTACTGTGCTCGTCATCCTCTGTTGGTTCGTGA	101		
Oy	775 GTACAGCTTCAGAGCAGCGAGGCGCATACGCTACTACCTTACCCAGAGTGACAAA	834		
Db	102 GTTACTTTCAGGGGCTCTATGATGGATTTTGTCTTCATCGTTCGACTTACTACAA	161		
Oy	835 TTGCAAACTGTAGATGATGATGAGCGGCGACATCCAGATTTTCTGCTGGGTGCC	894		
Db	162 CTACGACACCTCAGGATGAGCTTGATGCGCCTGTGCGAATCTTCTTCCCTCAGTCC	221		
Oy	895 GGGTTGGAAACCTACTGCGCTCTCCAGCTACAAACAAGTTCACAACTGTGCACAG	954		
Db	222 GCTGGGGAGGTCTCATCACCCTCTCATCCTACAAACAAGTTCACAACTGTGCACAG	281		
Oy	955 GACCGCTCATCACTTCTTATCACTGCTTGACCACTCTCTGCTGTTGCTCAAT	1014		
Db	282 GATCTGTGCTTGTAGCAACCTCAACCTGCTGACTATGCTTCTTGGCTTTGTGATC	341		
Db	1015 TTTCGCGTTTGGGGTATACGAGCGACGCTTAGAACAAGACATCGAGAGAGTGGGCTC	1074		
Db	342 TTCTCTATCGTGGTTTATATGCCCCAAGCTTAGGGCABAAGATGCTGATGTCATCGAC	401		
Oy	1075 GAAGCCCTTGACTGTTGTTGATCGTGTACCCGAGGCCATCGCCACCATGACGGCTCC	1134		
Db	402 TCAGAGATTGTGCTTGTCTTATTCATTCGCTTACCCCGAGGCCGCTCCCATGCGGTATCA	461		
Oy	1135 GTGTTTGGGCGCATCATCTTCTCTCATGCTTATTAACCTGGGACTGACATGACTTTT	1199		
Db	462 CCGCTGTGGGCGATCTCTTCTTCTTATTCATGTTGGTCCACCTCGCTGATCCCATGTC	521		
Oy	1195 GGAGGCTTTGAGGAGTACCAAGCGGCTTTTGGCAGCAATACCTCGAGTGTAGAGAGA	1254		
Db	522 AACATCATGAGAGAGGTGGTACACAGCCCTGTCGACGAGTTCGCCGACACCTCGCAG	581		
Oy	1255 CATCGCGAAGTATTTGGCTGTACCTGCTTGTTCATCTATATTTTGGCTCTGCCCAC	1314		
Db	582 AAGAAGACCTTCATCATGTTGGTGGGCTGTGACATCATGCTTCTCGATACAGTGC	641		
Oy	1315 ACCACATCGGTGGTGTATCTGCTGAGACTACTCATGTGTATGAGCCCTGGATTTGGCG	1374		
Db	642 ATCACAGAGGCTGAGCACTACTGGTCACTTTGATGAGGACTCTTATGAGAGCTGGGTTTCC	701		

0Y	1275	ATPCTATTCCGGAGTAATTGCTGAGAGCTCCGCGCGTCCGCTGGTATAGCGCTGCACCG	1435
Db	702	CTCATTAATGTTGGGCGCTTTGGCAACCATTTGGGCTCTCTCTCTATGTAACACGANGCT	761
0Y	1435	TTCTCTGAAGATGTGAGGACCATCTCTGGGCGACACC	1471
Db	762	TTC-CCAAATGACATTCGTACTATATCATCGGACCGCC	797
RESULT 9			
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603029220/F1 NIH_MGC_114		Human sapiens	cdna clone IMAGE:5199552 5'
LOCUS			
DEFINITION			
ACCESSION	B1756400		
VERSION	B1756400		
KEYWORDS	EST.		
SOURCE	human		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 836)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: c9apbs-r@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: LLML1499 row: p column: 01		
	High quality sequence stop: 816.		
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	/clone="IMAGE:5199552"		
	/clone_lib="NIH_MGC_114"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH MGC Library."		
BASE COUNT	148 a 251 c 221 g 216 t		
ORIGIN			
Query Match	13.1%;	Score 230.4;	DB 13; Length 836;
Best Local Similarity	61.5%;	Pred. No. 1e-49;	
Matches	369;	Conservative 0;	Mismatches 231; Indels 0; Gaps 0;
0Y	607	GGCCTGATGACATGAGGGCGCATCAAGCCGTGCTGTGTGTGTTGGGGTCTTTT	666
Db	96	GGCATTCATGACCTGGGCGCTCCCTGGCGCTGGAGCGGCGCTGTGCTCTGCGCC	155
0Y	667	GTCCTGCTACTTCTCTCTGTTGGAGAAAGCATCAGAGTCTGCTGCAAGTGTGGGTG	726
Db	156	GTCATCTGCTATTTCTTGATCTGTGAGGAGGGGTCAAGTCCACAGGCAAGTGCTTTATTTTC	215
0Y	727	ACACCTCTGAGCCCGTAGCTAGTGTGCTGTGATTTCTGCGAGAGGCGTCAAGCTTCCA	786
Db	216	ACAGCGACAGTTTCCGTACTGATGCTTGTATTTTTCGTGATCAGAGGTGTACACCTTCC	275
0Y	787	GGAGGACGAGGGGATACGCTACTACCTTAACCCAGAGTGGGACAAATTCGAAACCTCT	846



Db 276 GGAGCCCTACAGGAGCATCTACTACTTGAAACCCAGATTGTTCCCGCTCAAGGACCT 335  
 QY 847 AAGGATGATTTAGCCGGGATCCAGATTGTTCTTCGCTGGGTCGCCGGTTCCGGAACC 906  
 Db 336 CAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 395  
 QY 907 CTACTGCGCCCTCCAGCTACACAAGATTTCACACAGACTGCTACAGGAGCGGCTCATC 966  
 Db 396 CTGACAGCCCTGGGAGCTACACAAGATTTCACACAGACTGCTACAGGAGCGGCTCATC 455  
 QY 967 ACTTCTTATCACTGCTGACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026  
 Db 456 CTCTGCTCTTCCATCAAGTCCACAGCTTGTGGCGGGTGTGCTGCTTCCATCCAG 515  
 QY 1027 GGGTACATGGCGACCTTCCAGAACAGACATCGAGAGGTTGGCGCTCGAAGGCGCTGGA 1086  
 Db 516 GCGTTCATGTCCCAAGAGAGAGGGTCCCATTTTCTGAAGTGGCCAGTCAGAGTCTTGG 575  
 QY 1087 CTGGTGTTCATGCTGTATACCCGAGGACATCGCCACCATGACCGGCTCCGTTCTGGCC 1146  
 Db 576 CTGGCTTCATGCGCTTCCCAAGGCTGTGATGATGATGATGATGATGATGATGATGATGAT 635  
 QY 1147 ATCATCTTCTTCT 1206  
 Db 636 TGCCTGTCTTATCATGCTCATATTCCTAGAGGCTGACAGCCCACTGTCTGTGTGAG 695

RESULT 10  
 LOCUS B0941298 907 bp mRNA linear EST 21-AUG-2002  
 DEFINITION AGENCOUNT\_8859843 NCI\_CGAP\_Co24 Mus musculus cDNA clone  
 IMAGE:6475589 5', mRNA sequence.  
 ACCESSION B0941298  
 VERSION B0941298.1 GI:22356776  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (bases 1 to 907)  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM14014 row: j column: 06  
 High quality sequence stop: 665.  
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 /strain="FVB/N"  
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 /clone="IMAGE:6475589"  
 /clone\_lib="NCI\_CGAP\_Co24"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NCI;  
 Site: 2; Salt: cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 152 a 250 c 252 g 253 t  
 ORIGIN  
 Query Match 13.0%; Score 229.2; DB 14; Length 907;  
 Best Local Similarity 61.3%; Pred. No. 2.2e-49;  
 Matches 369; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 622 GGGCCGATCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681  
 Db 9 GGAGCCCTACACTGGAGGATGACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 68  
 QY 682 TCCCTTGGAAAGAGTCAAGAGTGTGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 741  
 Db 69 TGTGTGTGGAAAGGGGTCAAGTCAACAGAAAGATGTACTTCACTCTCATATCCCC 128  
 QY 742 TACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801  
 Db 129 TACGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 188  
 QY 802 ATACGCTACTACTTACCCAGAGTGGCAAAATTCGCAAACTAGTATGATGATGAC 861  
 Db 189 ATCATCTATCTCTCAAGCTAGCTGCTCAAAAGTATGAGTCCCTCAGGTATGATGAT 248  
 QY 862 GCGGATCCCAAGATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921  
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 QY 922 AGCTACAAAGTTCAACAAACAGTCTACAGGAGCCCTGATCACTCTCTCTATCAAC 981  
 Db 309 AGCTACAAAGTTCAACAAACAGTCTACAGGAGCCCTGATCACTCTCTCTATCAAC 368  
 QY 982 TGCCTGACCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1041  
 Db 369 AGCGGACCAAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428  
 QY 1042 GTTCAGAACAGACATCGAGAGTGGCCCTGCAAGCCCTGAGCTGCTTTCATCTG 1101  
 Db 429 GAGCAGGGTGTGCATATCTCCAAAGTGGCAGATCAGGGCTGCTTACCTTCATTTGCC 488  
 QY 1102 TACCCGAGGCCATGCGCCACATGACCGGCTCCGTTCTGGGCCCATCTTCTTCCGC 1161  
 Db 489 TACCCAGGGCTGTCTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548  
 QY 1162 ATGCTTATTAACCTGGAGCTTGAAGTCTTGGAGTCTTGGAGCAGTCAACAGGCT 1221  
 Db 549 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608  
 QY 1222 CT 1223  
 Db 609 CT 610

RESULT 11  
 LOCUS BM951745 660 bp mRNA linear EST 14-MAR-2002  
 DEFINITION UI-M-EG0-bup-P-03-0-UI.r1 NIH\_BMAP\_EG0 Mus musculus cDNA clone  
 IMAGE:5685362 5', mRNA sequence.  
 ACCESSION BM951745  
 VERSION BM951745.1 GI:19435335  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (bases 1 to 660)  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pyx-5.



FEATURES  
source

Location/Qualifiers  
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Site\_2: Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was size selected according to mRNA size fraction,  
ligated with Ecor I adaptor, digested with Not I, and then  
cloned directionally into pTX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is CAGCAGCAGC. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institute of Mental Health  
(NIMH), Hemlin Chin, Ph.D., program coordinator."

BASE COUNT  
136 a 186 c 170 g 168 t

Query Match 13.0%; Score 229; DB 14; Length 660;  
Best Local Similarity 62.4%; Pred. No. 2.1e-49;  
Matches 380; Conservative 0; Mismatches 220; Indels 9; Gaps 1;

468 GCTGCCATGACACCTGGACACAGAGTGAACAGCGCGTGTGACGCGGTACCC 527  
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52 GCTGCCCTGACACCTGACAGAACTCTTGAACTGCACTGCACTACTTCC 111  
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58 ACCTCAGA-----CTAATCTAATCTTCTACACCGCGGAGAGATTCTTGAC 578  
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112 CCAGAACACATCACCCTGACACATCCATCCACGTCACCTGCTGAGAGTTTACTTGG 171  
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579 TAAATATTGGACGACACAGTCTACAGGCTGATGACATGGGCGCATCAAGCCGC 638  
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172 CCATCTCCGAGATCATTCAAGAGGACTCCAGACCTGGGAGCATCAGTGGCA 231  
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639 GCTGCTCTGTGTGTTGGGGCTTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 698  
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232 GCTGCT 291  
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699 CAGGAGTGTGCAAGTGTGTGGGTGACACCTGCGCCGCTACGTTGCTGCTGAT 758  
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292 CAAACAGTGTGCAAGTGTGTGGGTGACACCTGCGCCGCTACGTTGCTGCTGAT 351  
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759 TGTGTGGCGAAGGCTTCACGCTCCAGAGCAGAGGCGCATACGTTACTACTTAC 818  
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352 CCTGCTGTGAGGAGGACCCCTCTCTGAGACCTGAGAGGGGTTGTTTACTTGA 411  
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819 CCAGAGTGTGCAAGTGTGTGGGTGACACCTGCGCCGCTACGTTGCTGCTGAT 878  
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412 ACCCACTGTGCAAGTGTGTGGGTGACACCTGAGAGGGGTTGTTTACTTGA 471  
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879 CTTCGTGCTGCTGCGGTGGAACCTCTACTGCGCTCTCAGCTACACAGTTTCA 938  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
472 TTTCCTCTGCGCGGGGTTTGGGTTCTCTGGGTTTGTAGTACAAAGTTCA 531  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
939 CAAACATGTCTACAGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 998  
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532 CAAACATGTCTACAGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591  
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999 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1058  
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RESULT 12  
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DEFINITION mRNA sequence.  
ACCESSION BE260823.1 GI:9132437  
VERSION BE260823.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE NIH-MGC  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov  
Plate: L1CMT175 row: h column: 17  
High quality sequence stop: 581.

FEATURES  
source

Location/Qualifiers  
1. 677  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3502912"  
/clone\_lib="NIH\_MGC\_19"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pORF7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: This is a NIH\_MGC library."

BASE COUNT  
129 a 187 c 185 g 176 t

Query Match 12.9%; Score 227.8; DB 10; Length 677;  
Best Local Similarity 63.3%; Pred. No. 4.5e-49;  
Matches 398; Conservative 0; Mismatches 227; Indels 4; Gaps 3;

597 CAAGTCTAAGGCTGTGATGACATGGGCGCATCAAGCCGTGCGCTCT- GTGTGTGT 655  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
1 CGAGACAGACGGGATTCATGACATCGCGCTGCCCGCAGCTCTCTCTCTCTCTCT 60  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
656 TCGGGGCTCTTCT 714  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
61 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
715 GTGTGTGAGGATGACAGCTGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
121 GTGTGTGATGACAGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
775 GTACGCTTTCAGAGGCGAGGAGCATATGCTACTACCTTACCCAGAGTGGCAAA 834  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
181 GTACGCTTTCAGAGGCGAGGAGCATATGCTACTACCTTACCCAGAGTGGCAAA 240  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
835 TTGCAAACTCTTAAGTATGATGAGGCGGATCCAGATTTTCTCTGCTGCTGCC 894  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
241 TTGAAAGAGCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT	13
BE868121	
LOCUS	644 bp mRNA
DEFINITION	BE868121 6014434339p1 NIH_MCC_65 Homo sapiens CDNA clone IMAGE:3847856 5', mRNA sequence.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9352 row: m column: 09  
High quality sequence stop:642.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1 IMAGE:3847856"
/clone_1b="NH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT      94 a      196 c      182 g      172 t
ORIGIN

```

[illegible][illegible]

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FEATURES
SOURCE
  Location/Qualifiers
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      /strain="FVB/N-3"
      /db_xref="taxon:10090"
      /clone="IMAGE:5391260"
      /clone_1id="NCI-CGAP_Mam2"
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